

PT Polynucleotide encoding a fusion polypeptide, useful for promoting differential function and influencing phenotype, comprises two subunits

Gencore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: April 28, 2005, 20:13:02 ; Search time 23.39 Seconds  
(without alignments)  
2830.147 Million cell updates/sec

Title: US-09-868-677-6

Perfect score: 3814

Sequence: 1 MSALLILAVGAARDCAD.....YFKGPSYSLRSTMTIRPLD 668

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*\*

1: p1r1:\*\*

2: p1r2:\*\*

3: p1r3:\*\*

4: p1r4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1263.5	33.1	330 1 GHU	Ig gamma-1 chain C
2	1259.5	33.0	374 2 S69339	Ig heavy chain V r
3	1255	32.9	255 4 S3166	Ig gamma-1 chain C
4	1230	31.7	234 2 PFO207	Ig gamma chain C r
5	1176	30.8	377 2 A23511	Ig gamma-3 chain C
6	1174	30.8	377 2 A60764	Ig gamma-3 chain C
7	1151	30.2	289 1 G3HUMI	Ig gamma-3 heavy C
8	1148	30.1	326 1 G2HU	Ig gamma-2 chain C
9	1141	29.9	337 1 G4HU	Ig gamma-4 chain C
10	928.5	24.3	323 1 GHRB	Ig gamma chain C r
11	915	24.0	328 2 I47160	Ig gamma 2b chain
12	915	24.0	328 2 I47159	Ig gamma 2a chain
13	911	23.9	277 2 I47162	Ig gamma 4 chain C
14	896	23.5	329 1 G2GP	Ig gamma-2 chain C
15	895	23.5	328 2 I47158	Ig gamma-1 chain C
16	886	23.2	328 2 I47161	Ig gamma 3 chain C
17	865.5	22.7	470 2 S22080	Ig heavy chain pre
18	861	22.6	329 1 G3MGC	Ig gamma-3 chain C
19	852	22.3	308 2 C30554	Ig heavy chain C r
20	852	22.3	472 2 S31459	Ig gamma-1 chain C
21	850	22.3	328 1 G3MGM	Ig gamma-3 chain C
22	843.5	22.1	444 2 PC4436	monoclonal antibody
23	842	22.1	333 2 PS0018	Ig gamma-2b chain
24	833.5	21.9	336 2 PS0017	Ig gamma-1 chain C
25	831.5	21.8	334 1 G1MS	Ig gamma-1 chain C
26	826.5	21.7	333 1 G1MGM	Ig gamma-1 chain C
27	818	21.4	469 2 S37483	Ig gamma-2a chain
28	812.5	21.3	330 1 G2MSA	Ig gamma-2a chain
29	812	21.3	329 2 S00847	Ig gamma-2c chain

30	807.5	21.2	339 1 G2MSAB	Ig gamma-2a chain
31	805	21.1	335 1 G2MSAB	Ig gamma-2a chain
32	797.5	20.9	446 2 S40295	Ig gamma-2a chain
33	794.5	20.8	322 2 PS0019	Ig gamma-2a chain
34	783.5	20.5	474 1 G2MS11	Ig gamma-2b chain
35	779	20.4	405 1 G2MSBM	Ig gamma-2b chain
36	773	20.3	475 2 S01321	Ig gamma-2b chain
37	770.5	20.2	327 2 S06611	Ig gamma-2 chain C
38	707	18.5	180 2 I46732	Ig gamma heavy Cha
39	577.5	15.1	249 2 S69340	Ig heavy chain VHI
40	574.5	15.1	218 2 A36040	Ig heavy chain V-I
41	571	15.0	152 2 S14236	Ig gamma-1 chain C
42	487	12.8	493 2 JC8027	type I angiotensin
43	486	12.7	312 2 JN0596	fibrinogen-related
44	477	12.5	866 2 D44234	fibrinogen alpha c
45	476	12.5	1810 1 A32230	tenascin precursor

## ALIGNMENTS

### RESULT 1

Ig gamma-1 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 31-Jan-1981 #sequence: rev18ion 18-Aug-1982 #ext change 09-Jul-2004

C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R/Billison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A/Reference number: A93433; PMID:82274238; PMID:6287432

A/Accession: A93433

A/Molecule type: DNA

A/Residues: 1-330 <EHL>

A/Cross-references: UNIPROT:P01857; EMBL:Z17370

A/Note: this sequence has the Gln117 allelic marker, 97-Lys, and the Gln(1) markers, ;

A/Note: Lys-330 is removed after translation

R/Harris, L.J.

submitted to the EMBL Data Library, October 1992

A/Reference number: S33904

A/Accession: S36861

A/Molecule type: DNA

A/Residues: 2-330 <HAR>

A/Cross-references: EMBL:Z17370

R/Takahashi, N.; Ueda, S.; Obata, M.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a

A/Reference number: S33887; PMID:83001943; PMID:6811139

A/Accession: S33887

A/Molecule type: DNA

A/Residues: 88-113;235-330 <TAK>

A/Cross-references: EMBL:Z17370

R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, G.M.

Biochemistry 9, 3161-3170, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A/Reference number: A90563; PMID:71064024; PMID:5489771

A/Accession: B90563

A/Molecule type: protein

A/Residues: 1-96; 'R', 98-135 <GUN>

A/Note: this sequence has the Gln(3) marker, 97-Arg

R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen

A/Reference number: A90564; PMID:71064025; PMID:5530842

A/Accession: B90564

A/Molecule type: protein

A/Residues: 136-154; 'Q', 156-165; 'Q', 167-176; 'O', 178-194; 'N', 196-197; 'D', 199-238; 'E', 240;

A/Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met

R/Ponstingl, H.; Hirschmann, N.

Hoppe-Seyler 8 Z. Physiol. Chem. 357, 1571-1604, 1976

A/Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nle)

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OM protein - protein search, using sw model

Run on: April 28, 2005, 20:01:26 ; Search time 98.5721 Seconds

(without alignments)  
3574.139 Million cell updates/sec

Title: US-09-868-677-6

Perfect score: 3814

Sequence: 1 MSALLILALVGAANVARDCAD.....YFKGPSYSTASTMIRPLD 688

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1372.5	33.4	679	2	Q96P08
2	1267.5	33.2	480	2	Q6N030
3	1267	33.2	473	2	Q6N054
4	1267	33.2	475	2	Q6P055
5	1265.5	33.2	470	2	Q6M206
6	1263.5	33.1	330	1	Q6PJA4
7	1263.5	33.1	465	2	GCL_HUMAN
8	1263.5	33.1	466	2	Q6GMA6
9	1263.5	33.1	469	2	Q6IN78
10	1263.5	33.1	470	2	Q725W1
11	1263.5	33.1	472	2	Q6N089
12	1263.5	33.1	475	2	Q6GMA7
13	1263.5	33.1	476	2	Q6GMA1
14	1262	33.1	473	2	Q6M2V7
15	1259.5	33.0	481	2	Q6N097
16	1259.5	33.0	482	2	Q72351
17	1257.5	33.0	348	2	Q6PYX1
18	1257.5	33.0	478	2	Q6PJA1
19	1257.5	33.0	480	2	Q6PJA1
20	1256.5	32.9	466	2	Q6N096
21	1252.5	32.8	544	2	Q6N095
22	1252.5	32.8	544	2	Q6PJA5
23	1245	32.6	487	2	Q65ZL2
24	1226.5	32.2	498	1	AGPI_HUMAN
25	1223	32.1	498	2	Q6C2F6
26	1220	32.0	498	1	AGPI_MOUSE
27	1219	32.0	498	1	AGPI_MOUSE
28	1217.5	31.9	521	2	Q6A0F0
29	1207.5	31.7	497	1	AGPI_RAT
30	1207.5	31.7	498	2	Q6BDY8
31	1176	30.8	354	2	Q6CTC2

32	1176	30.8	518	2	Q6N030	Q6N030 homo sapien
33	1172	30.7	521	2	Q6N4Y9	Q6N4Y9 homo sapien
34	1161	30.4	509	2	Q6N17	Q6N17 homo sapien
35	1156	30.3	290	1	GC3_HUMAN	P01860 homo sapien
36	1156	30.3	465	2	Q6P6C4	Q6P6C4 homo sapien
37	1148	30.1	326	1	GC2_HUMAN	P01859 homo sapien
38	1148	30.1	417	2	Q6N093	Q6N093 homo sapien
39	1146	30.0	464	2	Q6M2U6	Q6M2U6 homo sapien
40	1142.5	30.0	473	2	Q6TC63	Q6TC63 homo sapien
41	1141	29.9	327	1	GC4_HUMAN	P01861 homo sapien
42	1134	29.7	493	2	Q68CN4	Q68CN4 homo sapien
43	1133	29.7	481	1	AGPI_BOVIN	O18920 bos taurus
44	1132	29.7	476	2	Q6MZX7	Q6MZX7 homo sapien
45	1113.5	29.2	504	2	Q6GNY4	Q6GNY4 xenopus lae

## ALIGNMENTS

RESULT 1	ID	Q96P08	PRELIMINARY;	PRT;	679 AA.
AC	Q96P08				
DT	01-DEC-2001	(TREMBLrel. 19, Created)			
DT	01-JUN-2003	(TREMBLrel. 24, Last sequence update)			
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)			
DE	Factor VII active site mutant immunocjugate.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]	SEQUENCE FROM N.A.			
RP	MEHLIN=21477448; PubMed=11593034; DOI=10.1073/pnas.201420398;				
RX	Hu Z., Garen A.;				
RT	"Targeting tissue factor on tumor vascular endothelial cells and tumor				
RL	cells for immunotherapy in mouse models of prostatic cancer.";				
RN	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).				
RP	[2]	SEQUENCE FROM N.A.			
RA	Hu Z., Garen A.;				
RL	Submitted (FEB-2003) to the EMBL/Genbank/DBJ databases.				
DR	EMBL; AF272774; AAK58686.2; -.				
DR	HSSP; P08709; ICDI.				
DR	GO; GO:0005576; C:extracellular; IEA.				
DR	GO; GO:0005509; F:calcium ion binding; IEA.				
DR	GO; GO:0008233; F:peptidase activity; IEA.				
DR	GO; GO:0004295; F:trypsin activity; IEA.				
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.				
DR	InterPro; IPR00152; Abx_hydroxyl_S.				
DR	InterPro; IPR000742; EGF_2.				
DR	InterPro; IPR001881; EGF_Ca.				
DR	InterPro; IPR006209; EGF-like.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003597; Ig_C1.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	InterPro; IPR001254; Peptidase_S1.				
DR	InterPro; IPR009003; Pept_Ser_Cys.				
DR	InterPro; IPR000294; Vitk_dep_GLA.				
DR	Pfam; PF07654; C1-set; 2.				
DR	Pfam; PF00008; EGF_1.				
DR	Pfam; PF00594; GLA_1.				
DR	Pfam; PF00089; Trypsin; 1.				
DR	SMART; SM00179; EGF_CA; 1.				
DR	SMART; SM00069; GLA_1.				
DR	SMART; SM00407; IGCL_1.				
DR	SMART; SM00020; Tryp_SPC; 1.				
DR	PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.				
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.				
DR	PROSITE; PS01186; EGF_2; 1.				
DR	PROSITE; PS00026; EGF_3; 1.				
DR	PROSITE; PS01187; EGF_CA; 1.				
DR	PROSITE; PS00011; GLA_1; 1.				

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OM protein - protein search, using sw model

Run on: April 28, 2005, 20:17:28 ; Search time 78.1994 Seconds  
(without alignments)  
2931.049 Million cell updates/sec

Title: US-09-868-677-6  
Perfect score: 3814  
Sequence: 1 MSALLILALVGAANVARDCAD.....YKRGPSYLSRSTTMIRPD 688

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1426032 seqs, 333106140 residues  
Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubppa/PCT05\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubppa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1757	46.1	462	US-10-385-802-46	Sequence 46, Appl
2	1757	46.1	697	US-10-385-802-48	Sequence 48, Appl
3	1745	45.8	459	US-10-385-802-12	Sequence 12, Appl
4	1743.5	45.7	489	US-10-385-802-44	Sequence 44, Appl
5	1742	45.7	459	US-10-385-802-8	Sequence 8, Appl
6	1742	45.7	459	US-10-385-802-18	Sequence 18, Appl
7	1737	45.5	458	US-10-385-802-10	Sequence 10, Appl
8	1725.5	45.2	526	US-10-385-802-52	Sequence 52, Appl
9	1720.5	45.1	462	US-10-385-802-30	Sequence 30, Appl
10	1720.5	45.1	489	US-10-385-802-28	Sequence 28, Appl
11	1720.5	45.1	489	US-10-385-802-24	Sequence 24, Appl
12	1720.5	45.1	668	US-10-385-802-26	Sequence 26, Appl
13	1720.5	45.1	665	US-10-385-802-26	Sequence 26, Appl

14	1720.5	45.1	705	US-10-385-802-22	Sequence 22, Appl
15	1720.5	45.1	726	US-10-385-802-20	Sequence 20, Appl
16	1720.5	45.1	883	US-10-385-802-2	Sequence 2, Appl
17	1694	44.4	588	US-10-385-802-40	Sequence 40, Appl
18	1689	44.3	588	US-10-385-802-42	Sequence 42, Appl
19	1684	44.2	588	US-10-385-802-58	Sequence 58, Appl
20	1664	43.6	648	US-10-385-802-36	Sequence 36, Appl
21	1655.5	43.4	665	US-10-385-802-38	Sequence 38, Appl
22	1635.5	42.9	705	US-10-385-802-34	Sequence 34, Appl
23	1321	34.6	465	US-10-887-230-43	Sequence 43, Appl
24	1311	34.4	485	US-10-887-230-26	Sequence 26, Appl
25	1297.5	34.0	631	US-10-120-198B-2	Sequence 2, Appl
26	1295.5	34.0	949	US-10-233-838-19	Sequence 19, Appl
27	1292	33.9	452	US-09-773-877A-16	Sequence 16, Appl
28	1292	33.9	557	US-09-773-877A-14	Sequence 14, Appl
29	1290.5	33.8	462	US-09-773-877A-18	Sequence 18, Appl
30	1290.5	33.8	567	US-09-773-877A-12	Sequence 12, Appl
31	1290.5	33.8	567	US-09-773-877A-20	Sequence 20, Appl
32	1290.5	33.8	634	US-10-416-011-2	Sequence 2, Appl
33	1289	33.8	771	US-10-800-350-389	Sequence 389, App
34	1284	33.7	467	US-10-108-260A-4293	Sequence 4293, Ap
35	1283	33.6	464	US-10-938-353-102	Sequence 102, Appl
36	1282.5	33.6	470	US-10-887-230-14	Sequence 14, Appl
37	1282	33.6	711	US-10-071-485-90	Sequence 90, Appl
38	1281.5	33.6	731	US-09-825-012-46	Sequence 46, Appl
39	1281.5	33.6	741	US-09-825-012-55	Sequence 55, Appl
40	1281	33.6	476	US-09-747-669-3	Sequence 3, Appl
41	1281	33.6	476	US-10-290-703-3	Sequence 3, Appl
42	1281	33.6	499	US-10-207-655-15	Sequence 15, Appl
43	1281	33.6	499	US-10-207-655-148	Sequence 148, App
44	1281	33.6	499	US-10-053-530-15	Sequence 15, Appl
45	1280.5	33.6	500	US-10-207-655-240	Sequence 240, App

#### ALIGNMENTS

RESULT 1  
US-10-385-802-46  
Sequence 46, Application US/10385802  
Publication No. US20030224991A1  
GENERAL INFORMATION:  
APPLICANT: Dhanabal, Mohanraj  
APPLICANT: Larochele, William J.  
APPLICANT: Larochele, Henri  
APPLICANT: Wu, Frank  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND AMINO ACID SEQUENCES OF  
TITLE OF INVENTION: SECRETED PROTEINS INVOLVED IN ANGIOGENESIS  
FILE REFERENCE: 15966-5170B  
CURRENT APPLICATION NUMBER: US/10/385, 802  
CURRENT FILING DATE: 2003-03-11  
PRIOR APPLICATION NUMBER: 60/363,266  
PRIOR FILING DATE: 2002-03-11  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: Cnaseq version 0.1  
SEQ ID NO 46  
LENGTH: 462  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-385-802-46

Query Match 46.1%; Score 1757; DB 15; Length 462;  
Best Local Similarity 71.3%; Pred. No. 8.3e-123;  
Matches 331; Conservative 34; Mismatches 83; Indels 16; Gaps 4;  
QY 239 DKHTCPAPBELLGSPVLPAPPKKDTLMSRTPEYTCVVVDVSHDDPKYKFMVVD 298  
DB 1 DKHTCPAPBELLGSPVLPAPPKKDTLMSRTPEYTCVVVDVSHDDPKYKFMVVD 60  
QY 299 GVEVNAKTKPBEQVNSYRVVSVLTVAHQDLNKEKCKVSNKALPAPLEKTSKAK 358  
DB 61 GVEVNAKTKPBEQVNSYRVVSVLTVAHQDLNKEKCKVSNKALPAPLEKTSKAK 120

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OM protein - protein search, using sw model

Run on: April 28, 2005, 20:14:22 ; Search time 26.0631 Seconds  
(Without alignments)  
1970.544 Million cell updates/sec

Title: US-09-868-677-6  
3614

Perfect score: 1 MSALLITALVGAAYARDCAD.....YFKGYSYSLRTMMIRPLD 688

Sequence: BIOSUN62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Database : Issued Patents AA.\*  
Listing first 45 summaries

- 1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1292	33.9	452	US-09-773-877B-16	Sequence 16, Appl
2	1292	33.9	557	US-09-773-877B-14	Sequence 14, Appl
3	1290.5	33.8	462	US-09-773-877B-18	Sequence 18, Appl
4	1290.5	33.8	567	US-09-773-877B-12	Sequence 12, Appl
5	1290.5	33.8	567	US-09-773-877B-20	Sequence 20, Appl
6	1282	33.6	711	US-09-485-737B-90	Sequence 90, Appl
7	1282	33.6	711	US-10-071-485-90	Sequence 90, Appl
8	1280	33.6	476	US-08-487-550-4	Sequence 4, Appl
9	1280	33.6	476	US-09-526-098-4	Sequence 4, Appl
10	1280	33.6	476	US-09-383-916-4	Sequence 4, Appl
11	1276.5	33.5	622	US-09-499-846-2	Sequence 2, Appl
12	1275.5	33.4	911	US-08-484-438-10	Sequence 10, Appl
13	1275	33.4	859	US-09-313-942-7	Sequence 7, Appl
14	1274.5	33.4	497	US-09-499-846-6	Sequence 6, Appl
15	1274.5	33.4	525	US-09-499-846-4	Sequence 4, Appl
16	1272	33.4	396	US-08-784-512-3	Sequence 3, Appl
17	1272	33.4	396	US-09-176-228-3	Sequence 3, Appl
18	1272	33.4	450	US-09-996-288-216	Sequence 216, App
19	1272	33.4	450	US-09-996-288-218	Sequence 218, App
20	1272	33.4	450	US-09-996-288-250	Sequence 250, App
21	1272	33.4	476	US-08-487-550-12	Sequence 12, Appl
22	1272	33.4	476	US-09-526-098-12	Sequence 12, Appl
23	1272	33.4	476	US-09-383-916-12	Sequence 12, Appl
24	1270	33.3	977	US-09-590-656-1	Sequence 1, Appl
25	1270	33.3	977	US-09-733-764-1	Sequence 1, Appl
26	1269	33.3	437	PCT-US96-10043-11	Sequence 11, Appl
27	1269	33.3	592	US-09-313-942-8	Sequence 8, Appl

28	1268.5	33.3	277	US-09-428-082B-22	Sequence 22, Appl
29	1268	33.2	450	US-09-996-288-228	Sequence 228, App
30	1268	33.2	450	US-09-996-288-248	Sequence 248, App
31	1267.5	33.2	424	PCT-US95-03866-12	Sequence 12, Appl
32	1267.5	33.2	424	PCT-US95-03866-14	Sequence 14, Appl
33	1267	33.2	442	US-08-472-888A-7	Sequence 7, Appl
34	1267	33.2	442	PCT-US96-10043-9	Sequence 9, Appl
35	1266	33.2	475	US-09-740-002-27	Sequence 27, Appl
36	1265.5	33.2	450	US-09-996-288-208	Sequence 208, App
37	1265.5	33.2	451	US-09-996-288-230	Sequence 230, App
38	1265.5	33.2	951	US-09-313-942-9	Sequence 9, Appl
39	1265	33.2	253	US-09-428-082B-16	Sequence 16, Appl
40	1265	33.2	450	US-09-996-288-222	Sequence 222, App
41	1265	33.2	450	US-09-996-288-224	Sequence 224, App
42	1265	33.2	452	US-09-027-449-71	Sequence 71, Appl
43	1265	33.2	452	US-09-026-985-71	Sequence 71, Appl
44	1265	33.2	452	US-09-121-952A-71	Sequence 71, Appl
45	1265	33.2	452	US-09-234-340A-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1  
US-09-773-877B-16  
; Sequence 16, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710B  
; CURRENT APPLICATION NUMBER: US/09/773, 877B  
; NUMBER OF FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16  
; LENGTH: 452  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Filt(2-3 deltab)-Fc  
US-09-773-877B-16

Query Match 33.9%; Score 1292; DB 4; Length 452;  
Best Local Similarity 76.4%; Pred. No. 2.5e-107;  
Matches 259; Conservative 12; Mismatches 34; Indels 34; Gaps 9;

QY	137	LKHTGTAGKQSSLLTGADPSTADNDNCMKCAL	-----MLTGKWF-DACGPNLN-190
DB	138	LRGHT-----LVL-----NCTATPTNTRVQMT--WSYDEIDQSNHA 174	
QY	191	GMFV---TAGONHGLNGI-KMHYFKGYSYSLRTMMIRPLDGPQSPKSCDKTHTCPP 246	
DB	175	NIFSVLITIDMKQKDKGLTTCRVRSFSPKSVTSVTHIID-KAGPBPSCDKTHTCPP 233	
QY	247	CPABELLGSGSVFLFPKPKQDTLMISRTPEVTCVVDVSHEDPEVKENMYDVGEVNAK 306	
DB	234	CPABELLGSGSVFLFPKPKQDTLMISRTPEVTCVVDVSHEDPEVKENMYDVGEVNAK 293	
QY	307	TKPREBOYNSTRVSVLTVLHODMLNGKCYKCVSKALPAPLEKTIISRAKQPRREOV 366	
DB	294	TKPREBOYNSTRVSVLTVLHODMLNGKCYKCVSKALPAPLEKTIISRAKQPRREOV 353	
QY	367	YTLPPSDELTKQNVSLTCLVKGYFSDIAVEMESNQPENNYKTPPVLDSDGSFLYS 426	
DB	354	YTLPPSDELTKQNVSLTCLVKGYFSDIAVEMESNQPENNYKTPPVLDSDGSFLYS 413	
QY	427	KLIVDKSRMOQGVNFCVSHVBAALHNHYTQKSLSLSPGK 465	
DB	414	KLIVDKSRMOQGVNFCVSHVBAALHNHYTQKSLSLSPGK 452	

RESULT 2